

SEQUENCE LISTING

<110> Pausch, Mark H
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011

<141> 1997-03-11

<150> 08/332,312

<151> 1994-10-31

<150> PCT/US95/14364

<151> 1995-10-25

<160> 64

<170> PatentIn Ver. 2.1

<210> 1

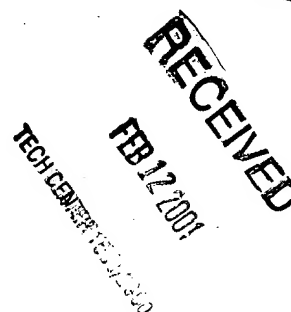
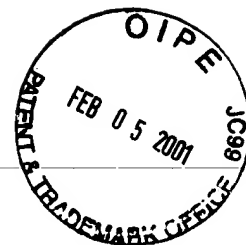
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<213> Drosophila melanogaster

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      20                   25                   30

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Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
      35                   40                   45

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Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
      50                   55                   60

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Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
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Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
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Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
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Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
115 120 125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
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Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
145 150 155 160

Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
165 170 175

Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
180 185 190

Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
195 200 205

Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr
210 215 220

Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
225 230 235 240

Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
245 250 255

Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
260 265 270

Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
275 280 285

Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
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Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
450 455 460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
465 470 475 480

Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
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Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
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Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
515 520 525

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545 550 555 560

Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
565 570 575

Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
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<212> DNA

<213> *Caenorhabditis elegans*

<400> 3

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atattgttct ccttgcttgg aatacctcta aacttggtta ccatcgctga cttggcaggt 240
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<213> *Drosophila melanogaster*

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Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
      35          40          45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
      50          55          60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly

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65		70		75		80
Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys						
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Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His						
	100		105		110	
Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile						
	115		120		125	
Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val						
	130		135		140	
Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser						
	145		150		155	160
Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly						
		165		170		175
Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu						
	180		185		190	
Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe						
	195		200		205	
Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val						
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Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln						
	225		230		235	240
Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val						
	245		250		255	
Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser						
	260		265		270	
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile						
	275		280		285	
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr						
	290		295		300	
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln						
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 <212> PRT
 <213> *Drosophila melanogaster*

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Arg Cys Val Thr Asp Glu Cys Pro
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 <211> 24
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 <213> *Drosophila melanogaster*

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<210> 9
<211> 24
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<213> Drosophila melanogaster

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Arg Tyr Ile Thr Asp His Cys Pro
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<210> 10
<211> 24
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<213> Drosophila melanogaster .

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Ile Ser Pro Thr Thr Phe Ala Gly
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<210> 11
<211> 24
<212> PRT

<213> Drosophila melanogaster

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Met Thr Pro Val Gly Phe Trp Gly
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<210> 12
<211> 24
<212> PRT

<213> Drosophila melanogaster

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15

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<213> Drosophila melanogaster

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<212> PRT

<213> Drosophila melanogaster

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Met Ala Pro Lys Thr Tyr Ile Gly

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<211> 24

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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<210> 18

<211> 24

<212> PRT

<213> Drosophila melanogaster

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<213> Drosophila melanogaster

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<210> 24
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<210> 25

<211> 24

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<213> Drosophila melanogaster

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<213> Drosophila melanogaster

<400> 26

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<210> 27

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<212> DNA

<213> Drosophila melanogaster

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<210> 31

<211> 24

<212> DNA

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24

<210> 32

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<210> 34

<211> 27

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<213> Drosophila melanogaster

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25

<210> 36
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 <212> DNA
 <213> *Caenorhabditis elegans*

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 <212> PRT
 <213> *Drosophila melanogaster*

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20	25	30	
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Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu			
35	40	45	
Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu			
50	55	60	
Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro			
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Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe			
	85	90	95
Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser			
100	105	110	
Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile			
115	120	125	
Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe			
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Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met			
145	150	155	160
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Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro			
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Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser			
195	200	205	
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210	215	220	
Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe			
225	230	235	240
Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly			
	245	250	255
Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys			

260	265	270
Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr		
275	280	285
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290	295	300
Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr		
305	310	315 320
Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp		
325	330	335
Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg		
340	345	350
Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly		
355	360	365
Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu		
370	375	380
Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu		
385	390	395 400
Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu		
405	410	415
Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser		
420	425	430
Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr		
435	440	445
Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu		
450	455	460
Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu		
465	470	475 480
Trp		

<210> 38
 <211> 337
 <212> PRT

<213> Caenorhabditis elegans

<220>

<221> UNSURE

<222> (337)

<223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38

Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser
1 5 10 15

Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
20 25 30

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly
65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe
195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40

rtcwccrwah ccdydg

18

<210> 41

<211> 28

<212> DNA

<213> Homo sapiens

<400> 41

cgcaggcaga gccacaaaga gtacacag

28

<210> 42

<211> 26

<212> DNA

<213> Homo sapiens

<400> 42

ggagatcagc taggcacdat atttgg

26

<210> 43

<211> 26

<212> DNA

<213> Homo sapiens

<400> 43

atgctgcatg cctcatgctt cccagc

26

<210> 44

<211> 20

<212> DNA

<213> Homo sapiens

<400> 44

ggttatttaa agagagggct

20

<210> 45

<211> 426

<212> PRT

<213> Homo sapiens

<400> 45

Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val

1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys
20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val
35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr
50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe
65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val
85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr
100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly
115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu
130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe
145 150 155 160

Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val
180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu
195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala
 245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr
 260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val
 275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu
 290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu
 305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val
 325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr
 340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu
 355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu
 370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu
 385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly
 405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
 420 425

<210> 46
 <211> 2130
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (35)
 <223> N AT POSITION 35 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2057)
 <223> N AT POSITION 2057 INDICATES UNDETERMINED

NUCLEOTIDE

<220>
 <221> unsure
 <222> (2067)
 <223> N AT POSITION 2067 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2111)
 <223> N AT POSITION 2111 INDICATES UNDETERMINED
 NUCLEOTIDE

<220>
 <221> unsure
 <222> (2120)
 <223> N AT POSITION 2120 INDICATES UNDETERMINED
 NUCLEOTIDE

<400> 46
 ccataccta acgactcact atagggctcg agcgnccgcc cgggcagtaa aatgcctgcc 60
 cgtgcagctc ggagcgcgca gcccgctctt gaataagaag tgagtacaat ggcgtgtttg 120
 taataaaaaag cttcaagtcc gtctttttca aaaaacattt tgaatgctgc atgcctcatg 180
 cttcccagcg cctcgcggga gagacccggc tatagagcag gaggggcggc acctgacttg 240
 ctggatccta aatctgccgc tcagaactcc aaaccgaggc tctcattttc cacgaaaccc 300
 acagtgttg cttcccgggt ggagagtgac acgaccatta atgttatgaa atggaagacg 360
 gtctccacga tattcctggt ggttgtcctc tatctgatca tcggagccac cgtgttcaaa 420
 gcattggagc agcctcatga gatttcacag aggaccacca ttgtgatcca gaagcaaaca 480
 ttcatatccc aacattcctg tgtcaattcg acggagctgg atgaactcat tcagcaaata 540
 gtggcagcaa taaatgcagg gattataccg ttaggaaaca cctccaatca aatcagtcac 600
 tgggatttgg gaagttcctt cttctttgct ggcactgtta ttacaaccat aggatttgga 660
 aacatctcac cacgcacaga aggcggcaaa atattctgta tcatctatgc cttactggga 720
 attcccctct ttggttttct cttggctgga gttggagatc agctaggcac catatttgga 780
 aaaggaattg ccaaagtgga agatacgtt attaatgga atgttagtca gaccaagatt 840
 cgcacatct caacaatcat atttatacta tttggctgtg tactctttgt ggctctgcct 900
 gcgatcatat tcaaacacat agaaggctgg agtgccctgg acgccattta tttgtggtt 960
 atcactctaa caactattgg atttggtgac tacgttgagc gtggatccga tattgaatat 1020
 ctggacttct ataagcctgt cgtgtggttc tggatccttg tagggcttgc ttactttgct 1080
 gctgtcctga gcatgattgg gagattggc cgagtgtat ctaaaaagac aaaagaagag 1140
 gtgggagagt tcagagcaca cgctgctgag tggacagcca acgtcacagc cgaattcaaa 1200
 gaaaccagga ggcgactgag tgtggagatt tatgacaagt tccagcgggc cacctccatc 1260
 aagcggaagc tctcggcaga actggctgga aaccacaatc aggagctgac tccttgtagg 1320

aggaccctgt cagtgaacca cctgaccagc gagagggatg tcttgccctcc cttactgaag 1380
 actgagagta tctatctgaa tggtttggcg ccacactgtg ctggtgaaga gattgctgtg 1440
 attgagaaca tcaaatagcc ctctctttta ataaccttag gcatagccat aggtgaggac 1500
 ttctctatgc tctttatgac tgttgctggt agcatttttt aaattgtgca tgagctcaaa 1560
 gggggaacaa aatagatata cccatcatgg tcatctatca tcaagagaat ttggaattct 1620
 gagccagcac tttctttctg atgatgcttg ttgaacggcc cactttcttt gatgagtggg 1680
 atgacaagca atgtctgatg cctttgtgtg ccagactgt tttcctctct ctttccctaa 1740
 tgtgccataa ggcctcagaa tgaattgaga attgtttctg gtaacaatgt agctttgagg 1800
 gatcagttct taacttttca ggtctacct aactgagcct agatatggac catttatgga 1860
 tgacaacaat tttttttttg taaatgacaa gaaattctta tgcagccttt tacctaagaa 1920
 atttctgtca gtgccttatc ttatgaagaa acagaacctc tctagctaata gtgtgggtttc 1980
 tcttccctg cccccaaccc taggctcacc tctgcagtct tttaccccag ttctcccatt 2040
 tgaataccat accttgntgg aaacagngtg taaaatgact gaagtgatga tgccgaagat 2100
 gaaatagatg ncaaattagn tggacattga 2130

<210> 47
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 47
 aaaagatcta aaatgcttcc cagcgcc

27

<210> 48
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 48
 aaagtcgacc tatttgatgt tctcaat

27

<210> 49
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 49
 aaaaagctta aaatgcttcc cagcgcc

27

<210> 50
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 50
aaatctagac tatttgatgt tctcaat

27

<210> 51
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (262)
<223> N AT POSITION 262 INDICATES UNDETERMINED
NUCLEOTIDE

<400> 51
aacaaaaacc ttttttgttt tgaatggcct agagagggta agggatcccc tgacgaacag 60
gagcagagcc agctagaacc tgggcctggc cagttcaagg ccaccagagg gcagccttct 120
gcggaaggca gtattggggt aggcaggac cccagcagac atggcactca gagctctcac 180
tgtccactga ctctctcttc tccaggttat ggccacatgg cccactatc gccaggcgga 240
aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300
accctgcgcc attgcctgct gcctgtgctc agccgccac gtgcctgggt agcgggtccac 360
tggcagctgt caccggccag ggctgcgctg ctgcaggcag ttgcactggg actgctggtg 420
gccagcagct ttgtgctgct gccagcgctg gtgctgtggg gccttcaggg cgactgcagc 480
ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52
<211> 956
<212> DNA
<213> Mus musculus

<400> 52
atgatacgat ttaatacgac tcaactatagg gaatttggcc ctcgaggcca agaattcggc 60
acgaggagaa tgtgcgcacg ttggctctca tcgtgtgcac cttcacctac ctgctggtgg 120
gcgccgcggg gttcgacgca ctggagtcgg agccggagat gatcgagcgg cagcggctgg 180
agctgcggca gctggagctg cgggcgcgct acaacctcag cgagggcggc tacgaggagc 240
tggagcgcgt cgtgctgcgc ctcaagccgc acaaggccgg cgtgcagtgg cgcttcgccg 300
gctccttcta cttcgccatc accgtcatca ccaccatcgg ctatggcat gcggcgcccc 360
gcacggacgg aggcaagggt ttctgcatgt tctacgcgct gctgggcatc ccgctcacac 420
tagtcatgtt ccagagcctg ggtgaacgca tcaacacctc cgtgaggtag ctgctgcacc 480
gtgccaaagag ggggctgggc atgcggcacg ccgaagtgtc catggccaac atggtgtctc 540
tcggtttcgt gtcgtgcac agcacgctgt gcatcggcgc agctgccttc tcctactacg 600
agcgtggac tttcttccag gcctattact actgcttcat caccctcacc accatcggt 660
tcggcgacta tgtggcgtg cagaaggacc aggcgtgca gacgcagccg cagtatgtgg 720
cttcagcttc gtgtacatcc tcacgggctc acggctcatg gcgcttcctc aacctcgtgg 780
tgctgcgatt catgaccatg aacgccgagg acgagaagcg tgatgcggag caccgcgccc 840
tgctcacgca caacggccag gctgtcggcc tgggtggcct gagctgcctg agcggtagcc 900

tgggcgacgg cgtgcgtccc cgcgaccag tcacatgcgc tgcggccgca agctta 956

<210> 53

<211> 1055

<212> DNA

<213> Mus musculus

<220>

<221> unsure

<222> (247)

<223> N AT POSITION 247 INDICATES UNDETERMINED
NUCLEOTIDE

<220>

<221> unsure

<222> (593)

<223> N AT POSITION 593 INDICATES UNDETERMINED
NUCLEOTIDE

<220>

<221> unsure

<222> (952)

<223> N AT POSITION 952 INDICATES UNDETERMINED
NUCLEOTIDE

<400> 53

ctgaaaccat gggcccgata cctgctcctg cttatggccc acctgctggc catgggcctt 60
ggggctgtgg tgcttcaggc cctggagggc cctccagctc gccacctcca ggcccaggtc 120
caggctgaac tggctagctt ccaggcagag cacagggcct gcttgccacc tgaggccctg 180
gaggagctgc taggtgcggt cctgagagca caggcccatg gagtttccag cctgggcaac 240
agctcanaga caagcaactg ggatctgccc tcagctctgc tgttcactgc cagcatcctc 300
accaccaccg gttatggcca catggcccca ctctcctcag gtggaaaaggc cttctgtgtg 360
gtctatgcag cccttgggct gccagcctct ctagcacttg tggctgccct gcgccactgc 420
ttgctgcctg tgttcagtcg cccagggtgac tgggtagcca ttcgctggca gctggcacca 480
gctcaggctg ctctgctaca ggcagcagga ctgggcctcc tgggtggcctg tgtcttcattg 540
ctgctgccag cactggtgct gtgggggtgta cagggtgact ggcagcctgc tanaaccatc 600
tacttctgtt tcggctcact cagcacgata ggcctaggag acttgctgcc tgcccatgga 660
cgtggcctgc acccagccat ttaccacctt gggcagtttg cacttcttgg ttacttgctc 720
ctggggctcc tggccatggt gtttagcagta gagaccttct cagagctgcc tcagggtccgt 780
gccatggtga aattcttttg gccagtggtc tctagaaccg atgaagatca agatggcatc 840
ctaggccaag atgagctggc tctgagcact gtgctgcctg acgccccagt cttgggacca 900
accaccccag cctgagcggg aggcaccaag gaggcttga agaacatagc angaagggtt 960
atgggaatga atatgtcatg ggataatgtt aattttaaaa attaatggg ctgcttagca 1020
tgcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1055

<210> 54

<211> 178
<212> PRT
<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 54

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
165 170 175

Leu Gly

<210> 55

<211> 309
 <212> PRT
 <213> Mus musculus

<400> 55

Gly	Ile	Trp	Pro	Ser	Arg	Pro	Arg	Ile	Arg	His	Glu	Glu	Asn	Val	Arg
1				5				10						15	
Thr	Leu	Ala	Leu	Ile	Val	Cys	Thr	Phe	Thr	Tyr	Leu	Leu	Val	Gly	Ala
			20					25					30		
Ala	Val	Phe	Asp	Ala	Leu	Glu	Ser	Glu	Pro	Glu	Met	Ile	Glu	Arg	Gln
		35					40					45			
Arg	Leu	Glu	Leu	Arg	Gln	Leu	Glu	Leu	Arg	Ala	Arg	Tyr	Asn	Leu	Ser
	50					55					60				
Glu	Gly	Gly	Tyr	Glu	Glu	Leu	Glu	Arg	Val	Val	Leu	Arg	Leu	Lys	Pro
65					70					75				80	
His	Lys	Ala	Gly	Val	Gln	Trp	Arg	Phe	Ala	Gly	Ser	Phe	Tyr	Phe	Ala
				85					90					95	
Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	His	Ala	Ala	Pro	Ser	Thr
			100					105					110		
Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe	Tyr	Ala	Leu	Leu	Gly	Ile	Pro
			115				120						125		
Leu	Thr	Leu	Val	Met	Phe	Gln	Ser	Leu	Gly	Glu	Arg	Ile	Asn	Thr	Ser
	130					135					140				
Val	Arg	Tyr	Leu	Leu	His	Arg	Ala	Lys	Arg	Gly	Leu	Gly	Met	Arg	His
145					150					155				160	
Ala	Glu	Val	Ser	Met	Ala	Asn	Met	Val	Leu	Ile	Gly	Phe	Val	Ser	Cys
				165					170					175	
Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala	Ala	Phe	Ser	Tyr	Tyr	Glu	Arg
			180				185						190		
Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile	Thr	Leu	Thr	Thr
		195					200					205			
Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu	Gln	Lys	Asp	Gln	Ala	Leu	Gln
	210					215				220					
Thr	Gln	Pro	Gln	Tyr	Val	Ala	Ser	Ala	Ser	Cys	Thr	Ser	Ser	Arg	Ala

225 230 235 240
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
 290 295 300

Ala Ala Ala Ser Leu
 305

<210> 56
 <211> 304
 <212> PRT
 <213> Mus musculus

<220>
 <221> UNSURE
 <222> (83)
 <223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

<220>
 <221> UNSURE
 <222> (198)
 <223> N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

<400> 56
 Leu Lys Pro Trp Ala Arg Tyr Leu Leu Leu Leu Met Ala His Leu Leu
 1 5 10 15

Ala Met Gly Leu Gly Ala Val Val Leu Gln Ala Leu Glu Gly Pro Pro
 20 25 30

Ala Arg His Leu Gln Ala Gln Val Gln Ala Glu Leu Ala Ser Phe Gln
 35 40 45

Ala Glu His Arg Ala Cys Leu Pro Pro Glu Ala Leu Glu Glu Leu Leu
 50 55 60

Gly Ala Val Leu Arg Ala Gln Ala His Gly Val Ser Ser Leu Gly Asn
 65 70 75 80

Ser Ser Xaa Thr Ser Asn Trp Asp Leu Pro Ser Ala Leu Leu Phe Thr
85 90 95

Ala Ser Ile Leu Thr Thr Thr Gly Tyr Gly His Met Ala Pro Leu Ser
100 105 110

Ser Gly Gly Lys Ala Phe Cys Val Val Tyr Ala Ala Leu Gly Leu Pro
115 120 125

Ala Ser Leu Ala Leu Val Ala Ala Leu Arg His Cys Leu Leu Pro Val
130 135 140

Phe Ser Arg Pro Gly Asp Trp Val Ala Ile Arg Trp Gln Leu Ala Pro
145 150 155 160

Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala
165 170 175

Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly
180 185 190

Asp Trp Gln Pro Ala Xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser
195 200 205

Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His
210 215 220

Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu
225 230 235 240

Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu
245 250 255

Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg
260 265 270

Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu
275 280 285

Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala
290 295 300

<210> 57

<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<221> VARIANT
<222> (1)..(9)
<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT
POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8
IS Y, F, V, I, M, OR L

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<400> 57

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
1 5

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>

<221> VARIANT
<222> (1)..(8)
<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,
S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I,
V, L, F, OR Y

<400> 58

Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa
1 5

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION

CHANNEL SEQUENCE

<400> 59

Tyr Ala Leu Leu Gly Ile Pro
1 5

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (6)

<223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60

Tyr Ala Leu Leu Gly Xaa Pro
1 5

<210> 61

<211> 178

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (88)

<223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser
1 5 10 15

Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe
20 25 30

Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly
35 40 45

Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr
50 55 60

Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly
 65 70 75 80

Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu
 85 90 95

Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg
 100 105 110

Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala
 115 120 125

Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe
 130 135 140

Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser
 145 150 155 160

Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly
 165 170 175

Leu Gly

<210> 62

<211> 309

<212> PRT

<213> Mus musculus

<400> 62

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg
 1 5 10 15

Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala
 20 25 30

Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln
 35 40 45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser
 50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro
 65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala

85

90

95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr
 100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro
 115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser
 130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His
 145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys
 165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg
 180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr
 195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln
 210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala
 225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr
 245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu
 260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser
 275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala
 290 295 300

Ala Ala Ala Ser Leu
 305

<210> 63

<211> 434

<212> PRT

<213> Caenorhabditis elegans

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala

1 5 10 15

Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val

20 25 30

Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro

35 40 45

Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp

50 55 60

Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro

65 70 75 80

Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro

85 90 95

Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu

100 105 110

Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser

115 120 125

Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn

130 135 140

Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp

145 150 155 160

Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys

165 170 175

Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn

180 185 190

Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val

195 200 205

Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp

210 215 220

Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala

225 230 235 240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn
 245 250 255

Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu
 260 265 270

Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly
 275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu
 290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val
 305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile
 325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Phe Cys Asn Tyr Arg
 340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe
 355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala
 370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg
 385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr
 405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser
 420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION
 CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,

S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,

L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro

1

5